

PATENT
Our Docket: P-LJ 4494

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:)
Reed and Sato) Group Art Unit: Unknown Yet
Serial No.: Pending) Examiner: Unknown Yet
Filed: Herewith) CERTIFICATE OF MAILING BY "EXPRESS MAIL"
For: CD40 ASSOCIATED) "EXPRESS MAIL" MAILING LABEL NUMBER: EL690155804US
PROTEINS) DATE OF DEPOSIT: January 9, 2001
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Commissioner for Patents
Washington, D.C. 20231

Sir:

Lijan Puthuvalil
(TYPED OR PRINTED NAME OF PERSON MAILING PAPER OR FEE)
[Signature]
(SIGNATURE OF PERSON MAILING PAPER OR FEE)

**REQUEST TO USE COMPUTER READABLE FORM OF SEQUENCE LISTING
FROM ANOTHER APPLICATION**

The computer readable form in the above-referenced application is identical with that filed in Application Number 08/349,357, filed December 2, 1994. In accordance with 37 CFR 1.821(e), please use the last-filed computer readable form filed in that application as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the computer readable form that will be used for the instant application. A paper copy of the Sequence Listing is included in a separately filed preliminary amendment for incorporation into the specification of the instant application.

The Commissioner is hereby authorized to charge payment of any fees associated with the filing submitted herewith or credit any overpayment to Deposit Account No. 03-0370. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

Date: January 9, 2001

[Signature]
Robert T. Ramos
Registration No. 37,915
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USPTO CUSTOMER NO. 23601

PATENT

Our Docket: P-LJ 4494

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Reed and Sato

Serial No.: Pending

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PROTEINS

BOX SEQUENCE

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Lijan Puthuvalil

(TYPED OR PRINTED NAME OF PERSON MAILING PAPER OR FEE)

(SIGNATURE OF PERSON MAILING PAPER OR FEE)

STATEMENT UNDER 37 C.F.R. § 1.821(f) and (g)

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR § 1.821(c) and (e), respectively, are the same. I hereby state that the paper and computer readable copies submitted herein are identical to those previously submitted on July 17, 1995, in U.S. Serial No. 08/349,357.

I hereby state that the submission, filed in accordance with 37 C.F.R. § 1.821(g) herein does not include new matter.

Respectfully submitted,

January 9, 2001

Date

Robert T. Ramos

Registration No. 37,915

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SEQUENCE LISTING

COPY

(1) GENERAL INFORMATION:

- (i) APPLICANT: Reed, John C.
Sato, Takaaki
- (ii) TITLE OF INVENTION: CD40 Associated Proteins
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell and Flores
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/349,357
 - (B) FILING DATE: 02-DEC-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-LJ 1203
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 137..1766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGAAGTGATG CCACTTGGTT AAGGTCCCAG AGCAGGTCAG AATCAGACCT AGGATCAGAA      60
ACCTGGCTCC TGGCTCCTGG CTCCCTACTC TTCTAAGGAT CGCTGTCCTG ACAGAAGAGA      120
ACTCCTCTTT CCTAAA ATG GAG TCG AGT AAA AAG ATG GAC TCT CCT GGC          169
          Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly
              1              5              10

GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG-CAC ACT GAC CGC AGT GCT          217
Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala
          15              20              25

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GGG Gly	ACG Thr	CCA Pro	GTT Val	TTT Phe	GTC Val	CCT Pro	GAA Glu	CAA Gln	GGA Gly	GGT Gly	TAC Tyr	AAG Lys	GAA Glu	AAG Lys	TTT Phe	265
		30					35					40				
GTG Val	AAG Lys	ACC Thr	GTG Val	GAG Glu	GAC Asp	AAG Lys	TAC Tyr	AAG Lys	TGT Cys	GAG Glu	AAG Lys	TGC Cys	CAC His	CTG Leu	GTG Val	313
	45					50					55					
CTG Leu	TGC Cys	AGC Ser	CCG Pro	AAG Lys	CAG Gln	ACC Thr	GAG Glu	TGT Cys	GGG Gly	CAC His	CGC Arg	TCC Ser	TGC Cys	GAG Glu	AGC Ser	361
	60				65					70					75	
TGC Cys	ATG Met	GCG Ala	GCC Ala	CTG Leu	CTG Leu	AGC Ser	TCT Ser	TCA Ser	AGT Ser	CCA Pro	AAA Lys	TGT Cys	ACA Thr	GCG Ala	TGT Cys	409
				80					85					90		
CAA Gln	GAG Glu	AGC Ser	ATC Ile	GTT Val	AAA Lys	GAT Asp	AAG Lys	GTG Val	TTT Phe	AAG Lys	GAT Asp	AAT Asn	TGC Cys	TGC Cys	AAG Lys	457
			95					100					105			
AGA Arg	GAA Glu	ATT Ile	CTG Leu	GCT Ala	CTT Leu	CAG Gln	ATC Ile	TAT Tyr	TGT Cys	CGG Arg	AAT Asn	GAA Glu	AGC Ser	AGA Arg	GGT Gly	505
		110					115					120				
TGT Cys	GCA Ala	GAG Glu	CAG Gln	TTA Leu	ACG Thr	CTG Leu	GGA Gly	CAT His	CTG Leu	CTG Leu	GTG Val	CAT His	TTA Leu	AAA Lys	AAT Asn	553
	125					130					135					
GAT Asp	TGC Cys	CAT His	TTT Phe	GAA Glu	GAA Glu	CTT Leu	CCA Pro	TGT Cys	GTG Val	CGT Arg	CCT Pro	GAC Asp	TGC Cys	AAA Lys	GAA Glu	601
	140				145					150					155	
AAG Lys	GTC Val	TTG Leu	AGG Arg	AAA Lys	GAC Asp	CTG Leu	CGA Arg	GAC Asp	CAC His	GTG Val	GAG Glu	AAG Lys	GCG Ala	TGT Cys	AAA Lys	649
				160					165					170		
TAC Tyr	CGG Arg	GAA Glu	GCC Ala	ACA Thr	TGC Cys	AGC Ser	CAC His	TGC Cys	AAG Lys	AGT Ser	CAG Gln	GTT Val	CCG Pro	ATG Met	ATC Ile	697
			175					180					185			
GCG Ala	CTG Leu	CAG Gln	AAA Lys	CAC His	GAA Glu	GAC Asp	ACC Thr	GAC Asp	TGT Cys	CCC Pro	TGC Cys	GTG Val	GTG Val	GTG Val	TCC Ser	745
		190					195					200				
TGC Cys	CCT Pro	CAC His	AAG Lys	TGC Cys	AGC Ser	GTC Val	CAG Gln	ACT Thr	CTC Leu	CTG Leu	AGG Arg	AGC Ser	GAG Glu	GGG Gly	ACA Thr	793
	205					210					215					
AAC Asn	CAG Gln	CAG Gln	ATC Ile	AAG Lys	GCC Ala	CAC His	GAG Glu	GCC Ala	AGC Ser	TCC Ser	GCC Ala	GTG Val	CAG Gln	CAC His	GTC Val	841
	220				225					230					235	
AAC Asn	CTG Leu	CTG Leu	AAG Lys	GAG Glu	TGG Trp	AGC Ser	AAC Asn	TCG Ser	CTC Leu	GAA Glu	AAG Lys	AAG Lys	GTT Val	TCC Ser	TTG Leu	889
				240				245						250		
TTG Leu	CAG Gln	AAT Asn	GAA Glu	AGT Ser	GTA Val	GAA Glu	AAA Lys	AAC Asn	AAG Lys	AGC Ser	ATA Ile	CAA Gln	AGT Ser	TTG Leu	CAC His	937
			255					260					265			
AAT Asn	CAG Gln	ATA Ile	TGT Cys	AGC Ser	TTT Phe	GAA Glu	ATT Ile	GAA Glu	ATT Ile	GAG Glu	AGA Arg	CAA Gln	AAG Lys	GAA Glu	ATG Met	985
		270					275					280				
CTT Leu	CGA Arg	AAT Asn	AAT Asn	GAA Glu	TCC Ser	AAA Lys	ATC Ile	CTT Leu	CAT His	TTA Leu	CAG Gln	CGA Arg	GTG Val	ATA Ile	GAC Asp	1033
	285					290					295					

CTCTGGGGGA TTTGAACCGG TCTGTCTTCA CTGAGGTCCT CGCGCTCAGA AAAGGACCTT 1866

GTGAGACGGA GGAAGCGGCA GAAGGCGGAC GCGTGCCGGC GGGAGGAGCC ACGCGTGAGA 1926

CACCTGACAC GTTTTATAAT AGACTAGCCA CACTTCACTC TGAAGAATTA TTTATCCTTC	1986
AACAAGCATA AATATTGCTG TCAGAGAAGG TTTTCATTTT CATTTTAAAA GATCTAGTTA	2046
ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTCTTC CTTAAACTTG	2106
AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT	2166
AAGTAAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAAATTCA	2226
AGAGTGCAAT TTTG	2240

(2) INFORMATION FOR SEQ ID NO:2:

. (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Ser	Ser	Lys	Lys	Met	Asp	Ser	Pro	Gly	Ala	Leu	Gln	Thr	Asn	1	5	10	15
Pro	Pro	Leu	Lys	Leu	His	Thr	Asp	Arg	Ser	Ala	Gly	Thr	Pro	Val	Phe	20	25	30	
Val	Pro	Glu	Gln	Gly	Gly	Tyr	Lys	Glu	Lys	Phe	Val	Lys	Thr	Val	Glu	35	40	45	
Asp	Lys	Tyr	Lys	Cys	Glu	Lys	Cys	His	Leu	Val	Leu	Cys	Ser	Pro	Lys	50	55	60	
Gln	Thr	Glu	Cys	Gly	His	Arg	Ser	Cys	Glu	Ser	Cys	Met	Ala	Ala	Leu	65	70	75	80
Leu	Ser	Ser	Ser	Ser	Pro	Lys	Cys	Thr	Ala	Cys	Gln	Glu	Ser	Ile	Val	85	90	95	
Lys	Asp	Lys	Val	Phe	Lys	Asp	Asn	Cys	Cys	Lys	Arg	Glu	Ile	Leu	Ala	100	105	110	
Leu	Gln	Ile	Tyr	Cys	Arg	Asn	Glu	Ser	Arg	Gly	Cys	Ala	Glu	Gln	Leu	115	120	125	
Thr	Leu	Gly	His	Leu	Leu	Val	His	Leu	Lys	Asn	Asp	Cys	His	Phe	Glu	130	135	140	
Glu	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys	Lys	Glu	Lys	Val	Leu	Arg	Lys	145	150	155	160
Asp	Leu	Arg	Asp	His	Val	Glu	Lys	Ala	Cys	Lys	Tyr	Arg	Glu	Ala	Thr	165	170	175	
Cys	Ser	His	Cys	Lys	Ser	Gln	Val	Pro	Met	Ile	Ala	Leu	Gln	Lys	His	180	185	190	
Glu	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	Val	Ser	Cys	Pro	His	Lys	Cys	195	200	205	
Ser	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	Gly	Thr	Asn	Gln	Gln	Ile	Lys	210	215	220	

Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu
 225 230 235 240
 Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
 245 250 255
 Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
 260 265 270
 Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
 275 280 285
 Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
 290 295 300
 Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu
 305 310 315 320
 Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
 325 330 335
 Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
 340 345 350
 Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
 355 360 365
 Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu
 370 375 380
 Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
 385 390 395 400
 Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
 405 410 415
 Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
 420 425 430
 Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
 435 440 445
 Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
 450 455 460
 Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
 465 470 475 480
 Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
 485 490 495
 Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
 500 505 510
 Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
 515 520 525
 Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
 530 535 540

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCAAA AAGGTGGCCA AG

22

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGATCATCAC TGTCTCTCCT GCAC

24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAATTCAAG GCCCCCCACC CCAAG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGATCAACTC TCTTTGCCAT CCTC

24

TGTCTCTCCT

25

25

27

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGATCCGCT ACCAACGGTG GAAG

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTCGACTCA TCTGAGAAGA CTGGG

25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAATACGACT CACTATAGGG AGACCACATG GATGATGTAT ATAACATCA TTTC

54

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTACCAGAAT TCGGCATGCC GGTAGAGGTG TGGTCA

36

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